

Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 117 KEELM 121

RESULT 3
071846
ribosomal protein L10 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
C:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12 #text_change 24 Sep 1999
C:Accession: 071846
A:Alm, R.A.; Ling, I.S.; Moir, D.T.; King, R.L.; Brown, R.D.; Doig, P.C.; Smith, D.R.;
Lives, C.; Gibson, R.; Moberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.F.; Vovis, C.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path-
A:Reference number: A71800; PMID:95120557; PMID:9523682
A:Accession: 071846
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <ARN>
A:Cross-references: GB:AE001540; GB:AE001449; NID:q4155717; PIDN:AA006701 1; PID:q415572
A:Experimental source: strain J99
C:Genetics:
A:Gene: rplJ
C:Superfamily: Escherichia coli ribosomal protein L10

Query Match 100.0%; Score 24; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 142 KEELM 136

RESULT 4
064669
ribosomal protein L10 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 13-Aug-1999
C:Accession: 064669
A:Tombs, J.F.; White, O.; Kervavag, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Taftus, H.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 549-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, F.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori
A:Reference number: A64520; PMID:97394467; PMID:9252185
A:Accession: 064669
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <TUM>
A:Cross-references: GB:AF000511; NID:q2314760; PIDN:AA008246 1; PID:q231436
C:Superfamily: Escherichia coli ribosomal protein L10

Query Match 100.0%; Score 24; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 142 KEELM 146

RESULT 5
060224
desrin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 24 Nov 1999

C:Accession: JE0223
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
submitted to JIPID, August 1998
A:Description: Complete amino acid sequences and phosphorylation sites, determined by
A:Reference number: JE0222
A:Accession: JE0223
A:Molecule type: protein
A:Residues: 1-164 <KAN>
C:Superfamily: cofilin
C:Keywords: acetylated amino end; phosphoprotein
F:18-33/Region: nuclear location signal
F:103-114/Region: actin binding #status predicted
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:2/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 24; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 95 KEELM 99

RESULT 6
A54184
desrin [validated] - human
N:Alternate names: actin depolymerizing factor (ADF)
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1994 #sequence_revision 02-Aug-1996 #text_change 15-Sep-2000
C:Accession: A54184
R:Hawkins, M.; Pope, B.; Maciver, S.K.; Weeds, A.G.
Biochemistry 32, 9985-9993, 1993
A:Title: Human actin depolymerizing factor mediates a pH-sensitive destruction of act
A:Reference number: A54184; PMID:94002009; PMID:8399167
A:Accession: A54184
A:Molecule type: mRNA
A:Residues: 1-165 <HAW>
A:Cross-references: GB:S65738; NID:q415586; PIDN:AA028361 1; PID:q415587
A:Experimental source: fetal brain
A:Note: sequence extracted from NCH backbone (NCBI:137963, NCBI:137964)
R:Hatanaka, H.; Moriyama, K.; Ogura, K.; Ichikawa, S.; Yahara, I.; Inagaki, F.
submitted to the Brookhaven Protein Data Bank, May 1997
A:Reference number: A59992; PDB:1AK6
A:Contents: annotation; conformation by (1)H-, (13)C-, and (15)N-NMR, residues 1-165
R:Hatanaka, H.; Ogura, K.; Moriyama, K.; Ichikawa, S.; Yahara, I.; Inagaki, F.
Cell 85, 1047-1055, 1996
A:Title: Tertiary structure of desrin and structural similarity between two actin-re
A:Reference number: A38990; PMID:96270507; PMID:8674111
A:Contents: annotation; NMR
C:Comment: The unphosphorylated form of desrin is capable of rapidly depolymerizing
C:Genetics:
A:Gene: GDB:ACTDP
A:Cross-references: GDB:249179
C:Superfamily: cofilin
C:Keywords: acetylated amino end; actin binding; phosphoprotein
F:2-165/Region: desrin #status predicted <MAP>
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F:3/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 96 KEELM 100

RESULT 7
A35179

destin - pig
 N:Alternate names: actin depolymerizing factor
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 03 Aug 1990 #sequence_revision 05 Aug 1994 #text_change 16 Jun 2000
 C:Accession: A35179
 P:Watanabe, K.; Nishida, E.; Yonekawa, N.; Sakai, H.; Matsumoto, S.; Iida, K.; Yahara, I.
 J. Biol. Chem. 265, 5768-5771, 1990
 A:Title: Destin, a mammalian actin-depolymerizing protein, is closely related to cofilin
 A:Reference number: A35179, MIM: 6020824, PMID: 2176824
 A:Accession: A35179
 A:Molecule type: mRNA
 A:Residues: 1-165 <MOR>
 A:Cross-references: GR P09074, OR P09076, NID g217681, PIRN AAA14185.1, PIR g217682
 A:Experimental source: brain
 C:Comment: Destin is an actin-binding protein that is capable of rapidly depolymerizing
 C:Superfamily: cofilin
 C:Keywords: acetylated amino end, actin binding, phosphoprotein
 F:26-36/Product: destin #status predicted
 F:104-134/Region: actin binding #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
 F:3/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0% Score 24, PR 1, Length 165
 Best Local Similarity 100.0% Pred. No. 1.4e+02
 Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 96 KEELM 100
 I I I I I

RESULT 8
 A35702
 N:Alternate names: actin-depolymerizing factor
 C:Species: Gallus gallus (chicken)
 C:Date: 12-Oct-1990 #sequence_revision 05 Aug 1994 #text_change 22 Jun 1999
 C:Accession: A35702, A35703, A40672
 R:Adams, M.E.; Minamide, L.S.; Duester, G.; Ramburg, J.R.
 Biochemistry 29, 7414-7420, 1990
 A:Title: Nucleotide sequence and expression of a cDNA encoding chick brain actin depolymerizing factor
 A:Reference number: A35702; MIM: 61027754; PMID: 2233773
 A:Accession: A35702
 A:Molecule type: mRNA
 A:Residues: 1-165 <ADA>
 A:Cross-references: GR g202912, NID g21056, PIRN AAA49575.1, PIR g21057
 A:Experimental source: brain
 A:Note: part of this sequence was confirmed by peptide sequencing
 R:Abu, H.; Endo, T.; Yamamoto, K.; Obinata, T.
 Biochemistry 29, 7420-7425, 1990
 A:Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic chick brain

A:Reference number: A35703; MIM: 61027755; PMID: 1699599
 A:Accession: A35703
 A:Molecule type: mRNA
 A:Residues: 1-165 <ARE>
 A:Cross-references: GR M6660, OR P02015, NID g21092, PIRN AAA49573.1, PIR g21093
 A:Experimental source: muscle
 A:Note: part of this sequence was confirmed by peptide sequencing
 P:Moran, T.F.; Lockert, F.; Minamide, L.S.; Brown, M.D.; Ramburg, J.R.
 J. Cell Biol. 122, 623-633, 1993
 A:Title: Isolation and characterization of a regulated form of actin depolymerizing factor

A:Reference number: A40672; MIM: 6128764, PMID: 7687605
 A:Accession: A40672
 A:Molecule type: protein
 A:Residues: 20-30 <MOR>
 R:Agnew, B.J.; Minamide, L.S.; Ramburg, J.R.
 J. Biol. Chem. 270, 17582-17587, 1995
 A:Title: Activation of phosphorylated actin depolymerizing factor and identification of phosphorylation site

A:Reference number: A38989; MIM: 61340558; PMID: 7615564
 A:Contents: annotation: acetylated amino end; phosphorylation site
 C:Comment: Destin is an actin-binding protein that is capable of rapidly depolymerizing

C:Superfamily: cofilin
 C:Keywords: acetylated amino end, actin binding, phosphoprotein
 F:26-36/Product: destin #status predicted
 F:104-134/Region: actin binding #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:3/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 100.0% Score 24, PR 1, Length 165
 Best Local Similarity 100.0% Pred. No. 1.4e+02
 Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 96 KEELM 100
 I I I I I

RESULT 9
 T28579
 N:Alternate names: variola major virus
 C:Species: variola major virus
 C:Date: 22 Oct 1999 #sequence_revision 22 Oct 1999 #text_change 21 Oct 2000
 C:Accession: T28579; J01840
 R:Massad, R.F.; Espinosa, I.; Liu, L.; Qi, J.; Minterbach, T.P.; Knight, J.C.; An
 Nature 366, 748-751, 1993
 A:Title: Potential virulence determinants in terminal regions of variola smallpox vir
 A:Reference number: T28579; MIM: 64086747, PMID: 8264798
 A:Accession: T28579
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-168 <MAS>
 A:Cross-references: MIM: 622579; NID g24595; PIRN AAA60869.1; PIR g40058
 A:Experimental source: strain Bangladesh 1975
 R:Agarwal, B.; Sulmes, J.P.; Smith, G.L.
 J. Gen. Virol. 73, 2887-2902, 1992
 A:Title: Nucleotide sequence of 21.8 kbp of variola major virus strain Harvey and com
 A:Reference number: J01840; MIM: 63057361; PMID: 1331292
 A:Accession: J01840
 A:Molecule type: DNA
 A:Residues: 1-168 <AGU>
 A:Cross-references: GR X75518, NID g418291, PIRN CAA47495.1, PIR J10232
 A:Experimental source: strain Harvey
 C:Keywords: glycoprotein, transmembrane protein
 F:15-34/Domain: transmembrane #status predicted
 F:133/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 100.0% Score 24, PR 2, Length 168
 Best Local Similarity 100.0% Pred. No. 1.4e+02
 Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 39 KEELM 43
 I I I I I

RESULT 10
 T42520
 N:Alternate names: vaccinia virus (strain Copenhagen)
 C:Species: vaccinia virus
 A:Note: Host Homo sapiens (man)
 C:Date: 10-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Nov-1997
 C:Accession: T42520
 R:Johnson, G.P.
 Submitted to GenBank, June 1990
 A:Reference number: A33172
 A:Accession: T42520
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-168 <JOH>
 C:Keywords: transmembrane protein

Query Match 100.0% Score 24; DB 2; Length 168;
 Best Local Similarity 100.0% Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5

Db 39 KEELM 43

RESULT 11

c72168

A:18R protein - variola minor virus (strain Garcia-1966)

C:Species: variola minor virus

C>Date: 24-Nov-1999 #sequence_revision 24 Nov-1999 #text_change 20 Jan 2000

C:Accession: G72168

R:Shchelkunov, S.N.; Tolmenin, A.V.; Gukorov, V.V.; Saifonov, P.F.; Massuna, R.F.; Lopad

submitted to GenBank, March 1998

A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor

A:Reference number: A72150

A:Accession: G72168

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <SHC>

A:Cross-references: GR:V16780; NID:95830555; PIDN:CAH54741 1; PID:95830702

A:Experimental source: strain Garcia-1966

C:Genetics:

A:Gene: A38R

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 168;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5

Db 39 KEELM 43

RESULT 12

T17420

EEV glycoprotein - vaccinia virus (strain Ankara)

C:Species: vaccinia virus

A:Variety: strain Ankara

C>Date: 21 Jan 2000 #sequence_revision 21 Jan 2000 #text_change 21 Jan 2000

C:Accession: T17420

R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.

submitted to the EMBL Data Library March 1997

A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain

A:Reference number: Z20877

A:Accession: T17420

A:Status: preliminary; translated from GR/EMBL/GenBank

A:Molecule type: DNA

A:Residues: 1-168 <ANT>

A:Cross-references: EMBL:U94848; PIDN:AAH96529.1

A:Experimental source: strain Ankara

C:Genetics:

A:Note: MVA145R

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 168;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5

Db 39 KEELM 43

RESULT 13

J01770

Sall4P protein precursor vaccinia virus (strain WR)

C:Species: vaccinia virus

C>Date: 30 Sep-1993 #sequence_revision 30 Sep-1993 #text_change 20-Jan-2000

C:Accession: J01770

R:Smith, G.L.; Chan, Y.S.; Howard, S.F.

J. Gen. Virol. 72, 1349-1376, 1991

A:Title: Nucleotide sequence of 428bp of vaccinia virus strain WR from near the right in

A:Reference number: J01767; MUID:91259983; PMID:2045793

A:Accession: J01770

A:Molecule type: DNA

A:Residues: 1-168 <SMI>

A:Cross-references: DDBJ:D11079; NID:9222717; PIDN:HAA01806.1; PID:9222721

C:Keywords: glycoprotein; transmembrane protein

F:1-36/Domain: signal sequence #status predicted <SIG>

F:37-168/Product: Sall4P protein #status predicted <MAT>

F:133/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 168;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5

Db 39 KEELM 43

RESULT 14

B36852

A:37R protein - variola virus

N:Alternate names: A34R protein

C:Species: variola virus

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-2001

C:Accession: B36852; S46864

R:Blinov, V.M.

submitted to GenBank, November 1992

A:Reference number: A36859

A:Accession: B36852

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <BLI>

A:Cross-references: GR:K69198; NID:9456758; PIDN:CAA49662 1; PID:9457032

A:Experimental source: strain India-1967, ssp. major, isolate Ind3

R:Kolykhalov, A.A.; Blinov, V.M.; Frolov, I.V.; Tolmenin, A.V.; Shchelkunov, S.N.; Sa

submitted to the EMBL Data Library, April 1992

A:Description: Nucleotide sequence analysis of the region of variola virus XhoI-E gen

A:Reference number: S46843

A:Accession: S46864

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <KOL>

A:Cross-references: EMBL:X7115; NID:9516412; PIDN:CAA47598.1; PID:9516424

A:Experimental source: strain India-1967, isolate Ind3

C:Keywords: transmembrane protein

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 168;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5

Db 39 KEELM 43

RESULT 15

167436

interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragmen

C:Species: Rattus norvegicus (Norway rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05 Nov-1999

C:Accession: 167436

R:Flaws, J.A.; Kogu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.L.; Hirschfield, A.N.;

Endocrinology 136, 5042-5053, 1995

A:Title: interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian

nucleosa cells of the ovarian follicle.

A:Reference number: 167436

A:Accession: 167436

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-182 <RES>

A:Cross-references: EMBL:U34684; NID:91004368; PIDN:AA052260.1; PID:91004369

Query Match 100.0%; Score 24; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
IIII
Db 153 KEELM 157

Search completed: January 16, 2003, 16:57:49
Job time : 10.2143 secs

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